SEQUENCE LISTING

(1) GENERAL INFORMATION:

   (i) APPLICANT: Tormo, Mar
                Tari, Ana M.
                Lopez-Berestein, Gabriel

  (ii) TITLE OF INVENTION: INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY LIPOSOMAL ANTISENSE OLIGODEOXYNUCLEOTIDES

 (iii) NUMBER OF SEQUENCES: 7

  (iv) CORRESPONDENCE ADDRESS:
     (A) ADDRESSEE: Arnold, White & Durkee
     (B) STREET: P.O. Box 4433
     (C) CITY: Houston
     (D) STATE: Texas
     (E) COUNTRY: United States of America
     (F) ZIP: 77210

   (v) COMPUTER READABLE FORM:
     (A) MEDIUM TYPE: Floppy disk
     (B) COMPUTER: IBM PC compatible
     (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

  (vi) CURRENT APPLICATION DATA:
     (A) APPLICATION NUMBER: US Unknown
     (B) FILING DATE: Concurrently Herewith
     (C) CLASSIFICATION: Unknown

 (viii) ATTORNEY/AGENT INFORMATION:
     (A) NAME: Wilson, Mark B.
     (B) REGISTRATION NUMBER: 37,259
     (C) REFERENCE/DOCKET NUMBER: UTXC:504

  (ix) TELECOMMUNICATION INFORMATION:
     (A) TELEPHONE: (512) 418-3000
     (B) TELEFAX: (512) 474-7577

(2) INFORMATION FOR SEQ ID NO:1:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 18 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGCGTGCGC CATCCTTC   18

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACGGTCCGCC ACTCCTTCCC   20

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 16 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGAAGGGCT TCTTCC   16

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 5086 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1459..2175

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCGCCCGCCC CTCCGCGCCG CCTGCCCGCC CGCCCGCCGC GCTCCCGCCC GCCGCTCTCC   60

GTGGCCCCGC CGCGCTGCCG CCGCCGCCGC TGCCAGCGAA GGTGCCGGGG CTCCGGGCCC   120

TCCCTGCCGG CGGCCGTCAG CGCTCGGAGC GAACTGCGCG ACGGGAGGTC CGGGAGGCGA   180

CCGTAGTCGC GCCGCCGCGC AGGACCAGGA GGAGGAGAAA GGGTGCGCAG CCCGGAGGCG   240

GGGTGCGCCG GTGGGGTGCA GCGGAAGAGG GGGTCCAGGG GGGAGAACTT CGTAGCAGTC   300

ATCCTTTTTA GGAAAAGAGG GAAAAAATAA AACCCTCCCC CACCACCTCC TTCTCCCCAC   360

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CCCTCGCCGC ACCACACACA GCGCGGGCTT CTAGCGCTCG GCACCGGCGG GCCAGGCGCG      420

TCCTGCCTTC ATTTATCCAG CAGCTTTTCG GAAAATGCAT TTGCTGTTCG GAGTTTAATC      480

AGAAGACGAT TCCTGCCTCC GTCCCCGGCT CCTTCATCGT CCCATCTCCC CTGTCTCTCT      540

CCTGGGGAGG CGTGAAGCGG TCCCGTGGAT AGAGATTCAT GCCTGTGTCC GCGCGTGTGT      600

GCGCGCGTAT AAATTGCCGA GAAGGGGAAA ACATCACAGG ACTTCTGCGA ATACCGGACT      660

GAAAATTGTA ATTCATCTGC CGCCGCCGCT GCCAAAAAAA AACTCGAGCT CTTGAGATCT      720

CCGGTTGGGA TTCCTGCGGA TTGACATTTC TGTGAAGCAG AAGTCTGGGA ATCGATCTGG      780

AAATCCTCCT AATTTTTACT CCCTCTCCCC CCGACTCCTG ATTCATTGGG AAGTTTCAAA      840

TCAGCTATAA CTGGAGAGTG CTGAAGATTG ATGGGATCGT TGCCTTATGC ATTTGTTTTG      900

GTTTTACAAA AAGGAAACTT GACAGAGGAT CATGCTGTAC TTAAAAAATA CAAGTAAGTC      960

TCGCACAGGA AATTGGTTTA ATGTAACTTT CAATGGAAAC CTTTGAGATT TTTTACTTAA     1020

AGTGCATTCG AGTAAATTTA ATTTCCAGGC AGCTTAATAC ATTGTTTTTA GCCGTGTTAC     1080

TTGTAGTGTG TATGCCCTGC TTTCACTCAG TGTGTACAGG GAAACGCACC TGATTTTTTA     1140

CTTATTAGTT TGTTTTTTCT TTAACCTTTC AGCATCACAG AGGAAGTAGA CTGATATTAA     1200

CAATACTTAC TAATAATAAC GTGCCTCATG AAATAAAGAT CCGAAAGGAA TTGGAATAAA     1260

AATTTCCTGC GTCTCATGCC AAGAGGGAAA CACCAGAATC AAGTGTTCCG CGTGATTGAA     1320

GACACCCCCT CGTCCAAGAA TGCAAAGCAC ATCCAATAAA ATAGCTGGAT TATAACTCCT     1380

CTTCTTTCTC TGGGGGCCGT GGGGTGGGAG CTGGGGCGAG AGGTGCCGTT GGCCCCCGTT     1440

GCTTTTCCTC TGGGAAGG ATG GCG CAC GCT GGG AGA ACG GGG TAC GAC AAC       1491
                    Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn
                     1                   5                   10

CGG GAG ATA GTG ATG AAG TAC ATC CAT TAT AAG CTG TCG CAG AGG GGC       1539
Arg Glu Ile Val Met Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly
              15                  20                  25

TAC GAG TGG GAT GCG GGA GAT GTG GGC GCC GCG CCC CCG GGG GCC GCC       1587
Tyr Glu Trp Asp Ala Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala
          30                  35                  40

CCC GCA CCG GGC ATC TTC TCC TCC CAG CCC GGG CAC ACG CCC CAT CCA       1635
Pro Ala Pro Gly Ile Phe Ser Ser Gln Pro Gly His Thr Pro His Pro
          45                  50                  55
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55

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GCC GCA TCC CGC GAC CCG GTC GCC AGG ACC TCG CCG CTG CAG ACC CCG     1683
Ala Ala Ser Arg Asp Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro
60                      65                  70                  75

GCT GCC CCC GGC GCC GCC GCG GGG CCT GCG CTC AGC CCG GTG CCA CCT     1731
Ala Ala Pro Gly Ala Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro
                    80                  85                  90

GTG GTC CAC CTG GCC CTC CGC CAA GCC GGC GAC GAC TTC TCC CGC CGC     1779
Val Val His Leu Ala Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg
                95                  100                 105

TAC CGC GGC GAC TTC GCC GAG ATG TCC AGC CAG CTG CAC CTG ACG CCC     1827
Tyr Arg Gly Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro
            110                 115                 120

TTC ACC GCG CGG GGA CGC TTT GCC ACG GTG GTG GAG GAG CTC TTC AGG     1875
Phe Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg
        125                 130                 135

GAC GGG GTG AAC TGG GGG AGG ATT GTG GCC TTC TTT GAG TTC GGT GGG     1923
Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly
140                 145                 150                 155

GTC ATG TGT GTG GAG AGC GTC AAC CGG GAG ATG TCG CCC CTG GTG GAC     1971
Val Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp
                160                 165                 170

AAC ATC GCC CTG TGG ATG ACT GAG TAC CTG AAC CGG CAC CTG CAC ACC     2019
Asn Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr
                175                 180                 185

TGG ATC CAG GAT AAC GGA GGC TGG GAT GCC TTT GTG GAA CTG TAC GGC     2067
Trp Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly
            190                 195                 200

CCC AGC ATG CGG CCT CTG TTT GAT TTC TCC TGG CTG TCT CTG AAG ACT     2115
Pro Ser Met Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr
        205                 210                 215

CTG CTC AGT TTG GCC CTG GTG GGA GCT TGC ATC ACC CTG GGT GCC TAT     2163
Leu Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr
220                 225                 230                 235

CTG AGC CAC AAG TGAAGTCAAC ATGCCTGCCC CAAACAAATA TGCAAAAGGT         2215
Leu Ser His Lys


TCACTAAAGC AGTAGAAATA ATATGCATTG TCAGTGATGT ACCATGAAAC AAAGCTGCAG   2275

GCTGTTTAAG AAAAAATAAC ACACATATAA ACATCACACA CACAGACAGA CACACACACA   2335

CACAACAATT AACAGTCTTC AGGCAAAACG TCGAATCAGC TATTTACTGC CAAAGGGAAA   2395
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TATCATTTAT TTTTTACATT ATTAAGAAAA AAGATTTATT TATTTAAGAC AGTCCCATCA    2455

AAACTCCGTC TTTGGAAATC CGACCACTAA TTGCCAAACA CCGCTTCGTG TGGCTCCACC    2515

TGGATGTTCT GTGCCTGTAA ACATAGATTC GCTTTCCATG TTGTTGGCCG GATCACCATC    2575

TGAAGAGCAG ACGGATGGAA AAAGGACCTG ATCATTGGGG AAGCTGGCTT TCTGGCTGCT    2635

GGAGGCTGGG GAGAAGGTGT TCATTCACTT GCATTTCTTT GCCCTGGGGG CGTGATATTA    2695

ACAGAGGGAG GGTTCCCGTG GGGGGAAGTC CATGCCTCCC TGGCCTGAAG AAGAGACTCT    2755

TTGCATATGA CTCACATGAT GCATACCTGG TGGGAGGAAA AGAGTTGGGA ACTTCAGATG    2815

GACCTAGTAC CCACTGAGAT TTCCACGCCG AAGGACAGCG ATGGGAAAAA TGCCCTTAAA    2875

TCATAGGAAA GTATTTTTTT AAGCTACCAA TTGTGCCGAG AAAAGCATTT TAGCAATTTA    2935

TACAATATCA TCCAGTACCT TAAACCCTGA TTGTGTATAT TCATATATTT TGGATACGCA    2995

CCCCCCAACT CCCAATACTG GCTCTGTCTG AGTAAGAAAC AGAATCCTCT GGAACTTGAG    3055

GAAGTGAACA TTTCGGTGAC TTCCGATCAG GAAGGCTAGA GTTACCCAGA GCATCAGGCC    3115

GCCACAAGTG CCTGCTTTTA GGAGACCGAA GTCCGCAGAA CCTACCTGTG TCCCAGCTTG    3175

GAGGCCTGGT CCTGGAACTG AGCCGGGCCC TCACTGGCCT CCTCCAGGGA TGATCAACAG    3235

GGTAGTGTGG TCTCCGAATG TCTGGAAGCT GATGGATGGA GCTCAGAATT CCACTGTCAA    3295

GAAAGAGCAG TAGAGGGGTG TGGCTGGGCC TGTCACCCTG GGGCCCTCCA GGTAGGCCCG    3355

TTTTCACGTG GAGCATAGGA GCCACGACCC TTCTTAAGAC ATGTATCACT GTAGAGGGAA    3415

GGAACAGAGG CCCTGGGCCT TCCTATCAGA AGGACATGGT GAAGGCTGGG AACGTGAGGA    3475

GAGGCAATGG CCACGGCCCA TTTTGGCTGT AGCACATGGC ACGTTGGCTG TGTGGCCTTG    3535

GCCACCTGTG AGTTTAAAGC AAGGCTTTAA ATGACTTTGG AGAGGGTCAC AAATCCTAAA    3595

AGAAGCATTG AAGTGAGGTG TCATGGATTA ATTGACCCCT GTCTATGGAA TTACATGTAA    3655

AACATTATCT TGTCACTGTA GTTTGGTTTT ATTTGAAAAC CTGACAAAAA AAAGTTCCA    3715

GGTGTGGAAT ATGGGGGTTA TCTGTACATC CTGGGGCATT AAAAAAAAAT CAATGGTGGG    3775

GAACTATAAA GAAGTAACAA AAGAAGTGAC ATCTTCAGCA AATAAACTAG GAAATTTTTT    3835

TTTCTTCCAG TTTAGAATCA GCCTTGAAAC ATTGATGGAA TAACTCTGTG GCATTATTGC    3895

ATTATATACC ATTTATCTGT ATTAACTTTG GAATGTACTC TGTTCAATGT TTAATGCTGT    3955

GGTTGATATT TCGAAAGCTG CTTTAAAAAA ATACATGCAT CTCAGCGTTT TTTTGTTTTT    4015
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AATTGTATTT AGTTATGGCC TATACACTAT TTGTGAGCAA AGGTGATCGT TTTCTGTTTG   4075

AGATTTTTAT CTCTTGATTC TTCAAAAGCA TTCTGAGAAG GTGAGATAAG CCCTGAGTCT   4135

CAGCTACCTA AGAAAAACCT GGATGTCACT GGCCACTGAG GAGCTTTGTT TCAACCAAGT   4195

CATGTGCATT TCCACGTCAA CAGAATTGTT TATTGTGACA GTTATATCTG TTGTCCCTTT   4255

GACCTTGTTT CTTGAAGGTT TCCTCGTCCC TGGGCAATTC CGCATTTAAT TCATGGTATT   4315

CAGGATTACA TGCATGTTTG GTTAAACCCA TGAGATTCAT TCAGTTAAAA ATCCAGATGG   4375

CGAATGACCA GCAGATTCAA ATCTATGGTG GTTTGACCTT TAGAGAGTTG CTTTACGTGG   4435

CCTGTTTCAA CACAGACCCA CCCAGAGCCC TCCTGCCCTC CTTCCGCGGG GGCTTTCTCA   4495

TGGCTGTCCT TCAGGGTCTT CCTGAAATGC AGTGGTCGTT ACGCTCCACC AAGAAAGCAG   4555

GAAACCTGTG GTATGAAGCC AGACCTCCCC GGCGGGCCTC AGGGAACAGA ATGATCAGAC   4615

CTTTGAATGA TTCTAATTTT TAAGCAAAAT ATTATTTTAT GAAAGGTTTA CATTGTCAAA   4675

GTGATGAATA TGGAATATCC AATCCTGTGC TGCTATCCTG CCAAAATCAT TTTAATGGAG   4735

TCAGTTTGCA GTATGCTCCA CGTGGTAAGA TCCTCCAAGC TGCTTTAGAA GTAACAATGA   4795

AGAACGTGGA CGTTTTTAAT ATAAAGCCTG TTTTGTCTTT TGTTGTTGTT CAAACGGGAT   4855

TCACAGAGTA TTTGAAAAAT GTATATATAT TAAGAGGTCA CGGGGGCTAA TTGCTAGCTG   4915

GCTGCCTTTT GCTGTGGGGT TTTGTTACCT GGTTTTAATA ACAGTAAATG TGCCCAGCCT   4975

CTTGGCCCCA GAACTGTACA GTATTGTGGC TGCACTTGCT CTAAGAGTAG TTGATGTTGC   5035

ATTTTCCTTA TTGTTAAAAA CATGTTAGAA GCAATGAATG TATATAAAAG C   5086

(2) INFORMATION FOR SEQ ID NO:5:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 239 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

    Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
    1   5   10   15

    Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
                20   25   30

```
Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
        35              40              45

Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
        50              55              60

Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
65              70              75              80

Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala
                85              90              95

Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe
        100             105             110

Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
        115             120             125

Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
        130             135             140

Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
145             150             155             160

Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
                165             170             175

Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
                180             185             190

Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
        195             200             205

Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala
        210             215             220

Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Ser His Lys
225             230             235
```

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 911 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 147..761

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

60

```
CAC ACC TGG ATC CAG GAT AAC GGA GGC TGG GTA GGT GCA TCT GGT GAT        749
His Thr Trp Ile Gln Asp Asn Gly Gly Trp Val Gly Ala Ser Gly Asp
                190                 195                 200
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```
GTG AGT CTG GGC TGAGGCCACA GGTCCGAGAT CGGGGGTTGG AGTGCGGGTG            801
Val Ser Leu Gly
                205
```

```
GGCTCCTGGG CAATGGGAGG CTGTGGAGCC GGCGAAATAA AATCAGAGTT GTTGCTTCCC      861

GGCGTGTCCC TACCTCCTCC TCTGGACAAA GCGTTCACTC CCAACCTGAC                 911
```

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 205 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
 1               5                  10                  15

Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
                20                  25                  30

Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
            35                  40                  45

Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
        50                  55                  60

Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
65                  70                  75                  80

Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala
                85                  90                  95

Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe
                100                 105                 110

Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
            115                 120                 125

Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
        130                 135                 140

Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
145                 150                 155                 160
```

Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
            165   170   175

5   Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
                180   185   190

    Gly Gly Trp Val Gly Ala Ser Gly Asp Val Ser Leu Gly
            195   200   205